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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 05 18:58:10 EDT 2007

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\*\*\*\*\*

Reviewer Comments:

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

The above <222> response denotes Xaa's at locations 2 through 4; however, "Pro" is at location 3. Same type of error throughout sequence 3 and sequence 43.

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

The <213> response above is erroneous; the response should only show "Homo sapiens." Please move "bromodomain peptide" to the <220>-<223> section.

<210> 34

<211> 112

<212> PRT

<213> Description of unknown organism, see Jeanmougin et al.,  
Trends in Biochem. Sci. 22:151-153 (1997)

Per 1.823 of Sequence Rules, the only valid <213> response is "Unknown";  
do not include any other explanation on the <213> line. The "see  
Jeanmougin..." is not a valid explanation of "Unknown." Please give the  
source of the genetic material in the <220>-<223> section. Same error  
in sequence 35.

\*\*\*\*\*

Application No: 09510314 Version No: 1.0

Input Set:

Output Set:

**Started:** 2007-06-05 17:13:10.137  
**Finished:** 2007-06-05 17:13:14.253  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 116 ms  
**Total Warnings:** 6  
**Total Errors:** 19  
**No. of SeqIDs Defined:** 44  
**Actual SeqID Count:** 44

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
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**Input Set:**

**Output Set:**

**Started:** 2007-06-05 17:13:10.137  
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**Total Warnings:** 6  
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**Actual SeqID Count:** 44

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (44)

## SEQUENCE LISTING

<110> Zhou, Ming-Ming  
Aggarwal, Aneel

<120> Methods of Identifying Modulators of Bromodomains

<130> 2459-1-003

<140> 09510314

<141> 2007-06-05

<150> 09/510,314

<151> 2000-02-22

<160> 44

<170> PatentIn version 3.0

<210> 1

<211> 3014

<212> DNA

<213> Homo sapiens

<400> 1

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<211> 832
<212> PRT
<213> Homo sapiens

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<400> 2

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20 25 30

```

```

Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Ala Gly Gly
35 40 45

```

```

Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala
50 55 60

```

```

Glu Gly Pro Gly Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
65 70 75 80

```

```

Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
85 90 95

```

```

Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
100 105 110

```

```

Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile
115 120 125

```

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Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
130 135 140

```

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Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
145 150 155 160

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			180					185					190				
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Glu	Lys	Arg	Thr	Leu	Ile	Leu	Thr	His	Phe	Pro	Lys	Phe	Leu	Ser	Met		
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Glu	Gly	Ala	Thr	Leu	Met	Gly	Cys	Glu	Leu	Asn	Pro	Arg	Ile	Pro	Tyr	
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Thr	Glu	Phe	Ser	Val	Ile	Ile	Lys	Lys	Gln	Lys	Glu	Ile	Ile	Lys	Lys	
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Gln	Gln	Val	Lys	Ser	His	Gln	Ser	Ala	Trp	Pro	Phe	Met	Glu	Pro	Val	
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Lys	Arg	Thr	Glu	Ala	Pro	Gly	Tyr	Tyr	Glu	Val	Ile	Arg	Phe	Pro	Met	
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770 775 780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys  
785 790 795 800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu  
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Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys  
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<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be  
any amino acid. One may be missing.

<220>

<221> Xaa

<222> (4)..(11)

<223> Xaa is a maximum of eight amino acids. Each of these can be  
any amino acid. One, two, or three may be missing.

<220>

<221> Xaa

<222> (5)..(5)

<223> Xaa is a single amino acid that is either Pro, Lys, or His.

<220>

<221> Xaa

<222> (6)..(6)

<223> Xaa is any single amino acid.

<220>

<221> Xaa

<222> (8)..(8)

<223> Xaa is a single amino acid that can be either Tyr, Phe, or His.

<220>

<221> Xaa

<222> (9)..(13)

<223> Xaa is any amino acid.

<220>  
<221> Xaa  
<222> (15)..(15)  
<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

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1 5 10 15

<210> 4  
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<221> Xaa  
<222> (6)..(6)  
<223> Xaa represents an acetyl-lysine

<400> 4

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<210> 6  
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<222> (8)..(8)

<223> Xaa represents an acetyl lysine.

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<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser  
1 5 10 15

Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu  
20 25 30

Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser  
35 40 45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr  
50 55 60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn  
65 70 75 80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn  
85 90 95

Ile Leu Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly  
100 105 110

<210> 8

<211> 110

<212> PRT

<213> Homo sapiens

<400> 8

Gly Lys Glu Leu Lys Asp Pro Asp Gln Leu Tyr Thr Thr Leu Lys Asn  
1 5 10 15

Leu Leu Ala Gln Ile Lys Ser His Pro Ser Ala Trp Pro Phe Met Glu  
20 25 30

Pro Val Lys Lys Ser Glu Ala Pro Asp Tyr Tyr Glu Val Ile Arg Phe

35

40

45

Pro Ile Asp Leu Lys Thr Met Thr Glu Arg Leu Arg Ser Arg Tyr Tyr  
 50 55 60

Val Thr Arg Lys Leu Phe Val Ala Asp Leu Gln Arg Val Ile Ala Asn  
 65 70 75 80

Cys Arg Glu Tyr Asn Pro Pro Asp Ser Glu Tyr Cys Arg Cys Ala Ser  
 85 90 95

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly  
 100 105 110

&lt;210&gt; 9

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Tetrahymena thermophila

&lt;400&gt; 9

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 20 25 30

Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro  
 35 40 45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val  
 50 55 60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala  
 65 70 75 80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu  
 85 90 95

Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys  
 100 105

&lt;210&gt; 10

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 10

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 20 25 30

Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro  
35 40 45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln  
50 55 60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys  
65 70 75 80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg  
85 90 95

Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro  
100 105

<210> 11

<211> 112

<212> PRT

<213> Homo sapiens

<400> 11

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Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln  
20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val  
35